In the Claims:

Kindly cancel claims 1, 16, 19, 21-23, 25-27, 32, 33, and 35 without prejudice to future prosecution.

Kindly enter the following new claims:

9.   (Amended)   A method for identifying [a] at least one potential target for antibacterial agents, comprising determining the bacterial target of [an] at least one uncharacterized bacteriophage inhibitor protein.

36.   (New) The method of claim 9, wherein said determining comprises identifying at least one bacterial protein which binds to said bacteriophage inhibitor protein.

37.   (New) The method of claim 36, wherein said binding is determined using affinity chromatography on a solid matrix.

38.   (New) The method of claim 9, wherein said determining comprises identifying at least one protein:protein interaction using a genetic screen.

39.   (New) The method of claim 38, wherein said genetic screen is a yeast two-hybrid screen.

40.   (New) The method of claim 9, wherein said determining comprises a co-immunoprecipitation assay or a protein-protein crosslinking assay.

41.   (New) The method of claim 9, wherein said determining comprises identifying a mutated bacterial coding sequence which protects a bacterium from said bacteriophage inhibitor.

42.   (New) The method of claim 9, wherein said determining comprises identifying a bacterial coding sequence which protects a bacterium against said bacteriophage inhibitor when expressed at high levels in said bacterium.

43.   (New) The method of claim 9, wherein said determining further comprises identifying a bacterial nucleic acid sequence encoding a polypeptide target of said bacteriophage inhibitor protein.

44.   (New) The method of claim 43, wherein said nucleic acid sequence is identified by determining at least a portion of the amino acid sequence of a bacterial protein target, and identifying a bacterial nucleic acid sequence which encodes said protein target.

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45.   (New) The method of claim 9, wherein said bacterial target is naturally produced by a bacterial species selected from the group consisting of species of the genera listed in Table 1.

46.   (New) The method of claim 9, wherein said bacterial target is naturally produced by a bacterial strain selected from the group consisting of species listed in Table 1.

47.   (New) The method of claim 9, wherein said inhibitor protein is naturally produced by a bacteriophage selected from the group consisting of uncharacterized bacteriophage listed in Table 1.

48.   (New) The method of claim 9, further comprising identifying a bacteriophage ORF which encodes a product having a bacteria-inhibiting function.

49.   (New) The method of claim 48, wherein said identifying a phage ORF comprises expressing at least one bacteriophage ORF in a bacterium, wherein inhibition of said bacterium following said expression is indicative that said ORF encodes a bacteria-inhibiting function.

50.   (New) The method of claim 49, wherein a plurality of bacteriophage ORFs are expressed in at least one bacterium.

51.   (New) The method of claim 50, wherein each of said plurality of bacteriophage ORFs is expressed in a different bacterium.

52.   (New) The method of claim 49, wherein said plurality of bacteriophage ORFs comprises at least 10% of the ORFs in the genome of said bacteriophage.

53.   (New) The method of claim 9, wherein said determining the bacterial target of a bacteriophage inhibitor protein is performed for a plurality of different bacteriophage of the same host bacterium.

54.   (New) The method of claim 9, wherein said bacterial target originates from an animal pathogen.

55.   (New) The method of claim 54, wherein said bacterial target is a gene homologous to a gene from an animal pathogen.

56.   (New) The method of claim 54, wherein said pathogen is a human pathogen.

57.   (New) The method of claim 9, wherein said bacterial target originates from a plant pathogen.

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58. (New) The method of claim 9, wherein said bacterial target is a gene homologous to a gene from a plant pathogen.

59. (New) The method of claim 9, further comprising determining the cellular or biochemical function or both of said inhibitor protein.

60. (New) The method of claim 9, wherein said identifying the bacterial target comprises identifying a phage-specific site of action.

61. (New) The method of claim 9, wherein said determining comprises identifying at least one bacterial protein which binds to a fragment of said bacteriophage inhibitor protein.

62. (New) The method of claim 61, wherein said fragment is at least 5 amino acids in length.

63. (New) The method of claim 61, wherein said fragment is at least 10 amino acids in length.

64. (New) The method of claim 61, wherein said fragment is at least 20 amino acids in length.

65. (New) The method of claim 45, wherein said bacterial species is *Staphylococcus aureus.*

66. (New) The method of claim 45, wherein said bacterial species is *Pseudomonas aeruginosa.*

67. (New) The method of claim 45, wherein said bacterial species is *Enterococcus faecalis.*

68. (New) The method of claim 45, wherein said bacterial species is *Enterococcus faecium.*

69. (New) The method of claim 45, wherein said bacterial species is *Haemophilus influenzae.*

70. (New) The method of claim 45, wherein said bacterial species is *Mycobacterium tuberculosis.*

71. (New) The method of claim 45, wherein said bacterial species is *Salmonella typhimumium.*

72. (New) The method of claim 45, wherein said bacterial species is *Streptococcus pneumoniae.*

73. (New) The method of claim 45, wherein said bacterial species is *Vibrio cholerae.*

74. (New) The method of claim 49, wherein said plurality of ORFs comprises at least at least 60% of the ORFs in the genome of said bacteriophage.

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75.   (New) The method of claim 49, wherein said plurality of ORFs comprises at least at least 80% of the ORFs in the genome of said bacteriophage.

76.   (New) The method of claim 50, wherein said plurality of bacteriophage ORFs are from a plurality of different bacteriophage.

77.   (New) The method of claim 76, wherein said plurality of different bacteriophage includes at least 5 bacteriophage.

78.   (New) The method of claim 76, wherein said plurality of different bacteriophage includes at least 10 different bacteriophage.

79.   (New) The method of claim 76, wherein said plurality of different bacteriophage includes at least 20 different bacteriophage.

80.   (New) The method of claim 76, wherein at least 10% of the genome of each of said plurality of different bacteriophage is expressed.

81.   (New) The method of claim 76, wherein at least 60% of the genome of each of said plurality of different bacteriophage is expressed.

82.   (New) The method of claim 76, wherein at least 80% of the genome of each of said plurality of different bacteriophage is expressed.

83.   (New) The method of claim 78, wherein at least 10% of the genome of each of said at least 10 different bacteriophage is expressed.

84.   (New) The method of claim 78, wherein at least 60% of the genome of each of said at least 10 different bacteriophage is expressed.

85.   (New) The method of claim 78, wherein at least 80% of the genome of each of said at least 10 different bacteriophage is expressed.

86.   (New) The method of claim 76, wherein said plurality of different bacteriophage have different host species.

87.   (New) The method of claim 78, wherein said at least 10 different bacteriophage have different host species.

88.   (New) The method of claim 76, further comprising sequencing at least 40% of the genome of each of said plurality of different bacteriophage.

89.   (New) The method of claim 76, further comprising sequencing at least 80% of the genome of each of said plurality of different bacteriophage.

90.   (New) The method of claim 78, further comprising sequencing at least 40 of the genome of each of said at least 10 different bacteriophage.

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91.   (New) The method of claim 78, further comprising sequencing at least 80 of the genome of each of said at least 10 different bacteriophage.

92.   (New) The method of claim 9, further comprising sequencing nucleic acid sequence encoding a said bacterial target.

93.   (New) A method for identifying at least one potential target for antibacterial agents, comprising determining the bacterial target of at least one untargeted bacteriophage inhibitor protein.

94.   (New) The method of claim 93, wherein said determining comprises identifying at least one bacterial protein which binds to said bacteriophage inhibitor protein.

95.   (New) The method of claim 93, wherein said determining further comprises identifying a bacterial nucleic acid sequence encoding a polypeptide target of said bacteriophage inhibitor protein.

96.   (New) The method of claim 93, wherein said determining comprises identifying at least one bacterial protein which binds to a fragment of said bacteriophage inhibitor protein.

97.   (New) The method of claim 96, wherein said fragment is at least 5 amino acids in length.

98.   (New) The method of claim 96, wherein said fragment is at least 10 amino acids in length.

99.   (New) The method of claim 96, wherein said fragment is at least 20 amino acids in length.

REMARKS

In response to the Examiner's requirement that Applicant elect one of the claim sets corresponding to one of the identified inventions, Applicant has selected claim group II (claim 9) and cancelled the other claims. This selection and the cancellation of non-elected claims is made without prejudice to future prosecution, and does not constitute an admission that any of the cancelled subject matter is un-patentable. Applicant reserves the right to prosecute claims to such subject matter in any appropriate application.

Applicant has requested above the insertion of Table 15. Table 15 was included in the prior utility application 09/407,804, from which the present application claims priority, and which was incorporated by reference in its entirety as Table 6. Thus, entry of Table 15 does not constitute the introduction of new matter.

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